



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/829,250

DATE: 08/02/2004

TIME: 14:37:42

Input Set : N:\CrF3\RULE60\10829250.raw
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1 <110> APPLICANT: HATTORI, NORIAKI
 2 MURAKAMI, SEIJI
 3 <120> TITLE OF INVENTION: LUCIFERASE AND A METHOD FOR DETECTING INTRACELLULAR ATP
 USING THE
 4 SAME
 5 <130> FILE REFERENCE: 193582US-3524-7126-0 PCT
 6 <140> CURRENT APPLICATION NUMBER: US/10/829,250
 7 <141> CURRENT FILING DATE: 2004-04-22
 8 <150> PRIOR APPLICATION NUMBER: US/09/581,241
 9 <151> PRIOR FILING DATE: 2000-06-26
 10 <150> PRIOR APPLICATION NUMBER: JP97/361022
 11 <151> PRIOR FILING DATE: 1997-12-26
 12 <160> NUMBER OF SEQ ID NOS: 8
 13 <170> SOFTWARE: PatentIn version 3.2
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 17 <212> TYPE: DNA
 18 <213> ORGANISM: ARTIFICIAL SEQUENCE
 19 <220> FEATURE:
 20 <223> OTHER INFORMATION: SYNTHETIC DNA
 21 <400> SEQUENCE: 1
 22 tgttgtactt aagaaaggaa aat
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 30 <400> SEQUENCE: 2
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 34 <211> LENGTH: 1644
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Luciola lateralis
 37 <220> FEATURE:
 38 <221> NAME/KEY: CDS
 39 <222> LOCATION: (1)..(1644)
 40 <400> SEQUENCE: 3
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 42 Met Glu Asn Met Glu Asn Asp Glu Asn Ile Val Tyr Gly Pro Glu Pro
 43 1 5 10 15
 44 ttt tac cct att gaa gag gga tct gct gga gca caa ttg cgc aag tat
 45 Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Ala Gln Leu Arg Lys Tyr
 46 20 25 30

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47	atg gat cga tat gca aaa ctt gga gca att gct ttt act aac gca ctt	144
48	Met Asp Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr Asn Ala Leu	
49	35 40 45	
50	acc ggt gtc gat tat acg tac gcc gaa tac tta gaa aaa tca tgc tgt	192
51	Thr Gly Val Asp Tyr Thr Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys	
52	50 55 60	
53	cta gga gag gct tta aag aat tat ggt ttg gtt gat gga aga att	240
54	Leu Gly Glu Ala Leu Lys Asn Tyr Gly Leu Val Val Asp Gly Arg Ile	
55	65 70 75 80	
56	gcg tta tgc agt gaa aac tgt gaa gaa ttc ttt att cct gta tta gcc	288
57	Ala Leu Cys Ser Glu Asn Cys Glu Glu Phe Phe Ile Pro Val Leu Ala	
58	85 90 95	
59	ggg tta ttt ata ggt gtc ggt gtg gct cca act aat gag att tac act	336
60	Gly Leu Phe Ile Gly Val Ala Pro Thr Asn Glu Ile Tyr Thr	
61	100 105 110	
62	cta cgt gaa ttg gtt cac agt tta ggc atc tct aag cca aca att gta	384
63	Leu Arg Glu Leu Val His Ser Leu Gly Ile Ser Lys Pro Thr Ile Val	
64	115 120 125	
65	ttt agt tct aaa aaa gga tta gat aaa gtt ata act gta caa aaa acg	432
66	Phe Ser Ser Lys Lys Gly Leu Asp Lys Val Ile Thr Val Gln Lys Thr	
67	130 135 140	
68	gta act gct att aaa acc att gtt ata ttg gac agc aaa gtg gat tat	480
69	Val Thr Ala Ile Lys Thr Ile Val Ile Leu Asp Ser Lys Val Asp Tyr	
70	145 150 155 160	
71	aga ggt tat caa tcc atg gac aac ttt att aaa aaa aac act cca caa	528
72	Arg Gly Tyr Gln Ser Met Asp Asn Phe Ile Lys Lys Asn Thr Pro Gln	
73	165 170 175	
74	ggg ttc aaa gga tca agt ttt aaa act gta gaa gtt aac cgc aaa gaa	576
75	Gly Phe Lys Gly Ser Ser Phe Lys Thr Val Glu Val Asn Arg Lys Glu	
76	180 185 190	
77	caa gtt gct ctt ata atg aac tct tcg ggt tca acc ggt ttg cca aaa	624
78	Gln Val Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys	
79	195 200 205	
80	ggg gtg caa ctt act cat gaa aat ttg gtc act aga ttt tct cac gct	672
81	Gly Val Gln Leu Thr His Glu Asn Leu Val Thr Arg Phe Ser His Ala	
82	210 215 220	
83	aga gat cca att tat gga aac caa gtt tca cca ggc acg gct att tta	720
84	Arg Asp Pro Ile Tyr Gly Asn Gln Val Ser Pro Gly Thr Ala Ile Leu	
85	225 230 235 240	
86	act gta gta cca ttc cat cat ggt ttt ggt atg ttt act act tta ggc	768
87	Thr Val Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly	
88	245 250 255	
89	tat cta act tgt ggt ttt cgt att gtc atg tta acg aaa ttt gac gaa	816
90	Tyr Leu Thr Cys Gly Phe Arg Ile Val Met Leu Thr Lys Phe Asp Glu	
91	260 265 270	
92	gag act ttt tta aaa aca ctg caa gat tac aaa tgt tca agc gtt att	864
93	Glu Thr Phe Leu Lys Thr Leu Gln Asp Tyr Lys Cys Ser Ser Val Ile	
94	275 280 285	
95	ctt gta ccg act ttg ttt gca att ctt aat aga agt gaa tta ctc gat	912

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98	aaa tat gat tta tca aat tta gtt gaa att gca tct ggc gga gca cct	960		
99	Lys Tyr Asp Leu Ser Asn Leu Val Glu Ile Ala Ser Gly Gly Ala Pro			
100	305	310	315	320
101	tta tct aaa gaa att ggt gaa gct gtt gct aga cgt ttt aat tta ccg	1008		
102	Leu Ser Lys Glu Ile Gly Glu Ala Val Ala Arg Arg Phe Asn Leu Pro			
103	325	330	335	
104	ggg gtt cgt caa ggc tat ggt tta aca gaa aca acc tct gca att att	1056		
105	Gly Val Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Ile			
106	340	345	350	
107	atc aca ccg gaa ggc gat gat aaa cca ggt gct tct ggc aaa gtt gtg	1104		
108	Ile Thr Pro Glu Gly Asp Asp Lys Pro Gly Ala Ser Gly Lys Val Val			
109	355	360	365	
110	cca tta ttt aaa gca aaa gtt atc gat ctt gat act aaa aaa act ttg	1152		
111	Pro Leu Phe Lys Ala Lys Val Ile Asp Leu Asp Thr Lys Lys Thr Leu			
112	370	375	380	
113	ggc ccg aac aga cgt gga gaa gtt tgt gta aag ggt cct atg ctt atg	1200		
114	Gly Pro Asn Arg Arg Gly Glu Val Cys Val Lys Gly Pro Met Leu Met			
115	385	390	395	400
116	aaa ggt tat gta gat aat cca gaa gca aca aga gaa atc ata gat gaa	1248		
117	Lys Gly Tyr Val Asp Asn Pro Glu Ala Thr Arg Glu Ile Ile Asp Glu			
118	405	410	415	
119	gaa ggt tgg ttg cac aca gga gat att ggg tat tac gat gaa gaa aaa	1296		
120	Glu Gly Trp Leu His Thr Gly Asp Ile Gly Tyr Tyr Asp Glu Glu Lys			
121	420	425	430	
122	cat ttc ttt atc gtg gat cgt ttg aag tct tta atc aaa tac aaa gga	1344		
123	His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly			
124	435	440	445	
125	tat caa gta cca cct gct gaa tta gaa tct gtt ctt ttg caa cat cca	1392		
126	Tyr Gln Val Pro Pro Ala Glu Leu Glu Ser Val Leu Leu Gln His Pro			
127	450	455	460	
128	aat att ttt gat gcc ggc gtt gct ggc gtt cca gat cct ata gct ggt	1440		
129	Asn Ile Phe Asp Ala Gly Val Ala Gly Val Pro Asp Pro Ile Ala Gly			
130	465	470	475	480
131	gag ctt ccg gga gct gtt gta ctt aag aaa gga aaa tct atg act	1488		
132	Glu Leu Pro Gly Ala Val Val Leu Lys Lys Gly Lys Ser Met Thr			
133	485	490	495	
134	gaa aaa gaa gta atg gat tac gtt gct agt caa gtt tca aat gca aaa	1536		
135	Glu Lys Glu Val Met Asp Tyr Val Ala Ser Gln Val Ser Asn Ala Lys			
136	500	505	510	
137	cgt ttg cgt ggt gtc cgt ttt gtg gac gaa gta cct aaa ggt ctc	1584		
138	Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu			
139	515	520	525	
140	act ggt aaa att gac ggt aaa gca att aga gaa ata ctg aag aaa cca	1632		
141	Thr Gly Lys Ile Asp Gly Lys Ala Ile Arg Glu Ile Leu Lys Lys Pro			
142	530	535	540	
143	gtt gct aag atg	1644		
144	Val Ala Lys Met			

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145      545
147 <210> SEQ ID NO: 4
148 <211> LENGTH: 548
149 <212> TYPE: PRT
150 <213> ORGANISM: Luciola lateralis
151 <400> SEQUENCE: 4
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154 Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Ala Gln Leu Arg Lys Tyr
155   20          25          30
156 Met Asp Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr Asn Ala Leu
157   35          40          45
158 Thr Gly Val Asp Tyr Thr Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys
159   50          55          60
160 Leu Gly Glu Ala Leu Lys Asn Tyr Gly Leu Val Val Asp Gly Arg Ile
161   65          70          75          80
162 Ala Leu Cys Ser Glu Asn Cys Glu Glu Phe Phe Ile Pro Val Leu Ala
163   85          90          95
164 Gly Leu Phe Ile Gly Val Gly Val Ala Pro Thr Asn Glu Ile Tyr Thr
165   100         105         110
166 Leu Arg Glu Leu Val His Ser Leu Gly Ile Ser Lys Pro Thr Ile Val
167   115         120         125
168 Phe Ser Ser Lys Lys Gly Leu Asp Lys Val Ile Thr Val Gln Lys Thr
169   130         135         140
170 Val Thr Ala Ile Lys Thr Ile Val Ile Leu Asp Ser Lys Val Asp Tyr
171   145         150         155         160
172 Arg Gly Tyr Gln Ser Met Asp Asn Phe Ile Lys Lys Asn Thr Pro Gln
173   165         170         175
174 Gly Phe Lys Gly Ser Ser Phe Lys Thr Val Glu Val Asn Arg Lys Glu
175   180         185         190
176 Gln Val Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys
177   195         200         205
178 Gly Val Gln Leu Thr His Glu Asn Leu Val Thr Arg Phe Ser His Ala
179   210         215         220
180 Arg Asp Pro Ile Tyr Gly Asn Gln Val Ser Pro Gly Thr Ala Ile Leu
181   225         230         235         240
182 Thr Val Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly
183   245         250         255
184 Tyr Leu Thr Cys Gly Phe Arg Ile Val Met Leu Thr Lys Phe Asp Glu
185   260         265         270
186 Glu Thr Phe Leu Lys Thr Leu Gln Asp Tyr Lys Cys Ser Ser Val Ile
187   275         280         285
188 Leu Val Pro Thr Leu Phe Ala Ile Leu Asn Arg Ser Glu Leu Leu Asp
189   290         295         300
190 Lys Tyr Asp Leu Ser Asn Leu Val Glu Ile Ala Ser Gly Gly Ala Pro
191   305         310         315         320
192 Leu Ser Lys Glu Ile Gly Glu Ala Val Ala Arg Arg Phe Asn Leu Pro
193   325         330         335
194 Gly Val Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Ile

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195	340	345	350
196	Ile Thr Pro Glu Gly Asp Asp Lys Pro Gly Ala Ser Gly Lys Val Val		
197	355	360	365
198	Pro Leu Phe Lys Ala Lys Val Ile Asp Leu Asp Thr Lys Lys Thr Leu		
199	370	375	380
200	Gly Pro Asn Arg Arg Gly Glu Val Cys Val Lys Gly Pro Met Leu Met		
201	385	390	395
202	Lys Gly Tyr Val Asp Asn Pro Glu Ala Thr Arg Glu Ile Ile Asp Glu		
203	405	410	415
204	Glu Gly Trp Leu His Thr Gly Asp Ile Gly Tyr Tyr Asp Glu Glu Lys		
205	420	425	430
206	His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly		
207	435	440	445
208	Tyr Gln Val Pro Pro Ala Glu Leu Glu Ser Val Leu Leu Gln His Pro		
209	450	455	460
210	Asn Ile Phe Asp Ala Gly Val Ala Gly Val Pro Asp Pro Ile Ala Gly		
211	465	470	475
212	Glu Leu Pro Gly Ala Val Val Val Leu Lys Lys Gly Lys Ser Met Thr		
213	485	490	495
214	Glu Lys Glu Val Met Asp Tyr Val Ala Ser Gln Val Ser Asn Ala Lys		
215	500	505	510
216	Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu		
217	515	520	525
218	Thr Gly Lys Ile Asp Gly Lys Ala Ile Arg Glu Ile Leu Lys Lys Pro		
219	530	535	540
220	Val Ala Lys Met		
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227 <220>	FEATURE:		
228 <221>	NAME/KEY: CDS		
229 <222>	LOCATION: (1)..(1644)		
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234	ttt tac cct att gaa gag gga tct gct gga gca caa ttg cgc aag tat		96
235	Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Ala Gln Leu Arg Lys Tyr		
236	20 25 30		
237	atg gat cga tat gca aaa ctt gga gca att gct ttt act aac gca ctt		144
238	Met Asp Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr Asn Ala Leu		
239	35 40 45		
240	acc ggt gtc gat tat acg tac gcc gaa tac tta gaa aaa tca tgc tgt		192
241	Thr Gly Val Asp Tyr Thr Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys		
242	50 55 60		
243	cta gga gag gct tta aag aat tat ggt ttg gtt gat gga aga att		240
244	Leu Gly Glu Ala Leu Lys Asn Tyr Gly Leu Val Val Asp Gly Arg Ile		

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/02/2004
PATENT APPLICATION: US/10/829,250 TIME: 14:37:43

Input Set : N:\Crf3\RULE60\10829250.raw
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The rules require that a line not exceed 72 characters in length. This includes spaces.

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/829,250

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Input Set : N:\Crf3\RULE60\10829250.raw

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